AMENDMENTS TO THE CLAIMS

Listing of Claims:

This Listing of Claims will replace all prior versions, and listings, of claims in the application:

1. (Previously Presented) A method comprising:

a) aligning a biomolecule in a parallel manner on a surface by molecular combing;

b) imaging the biomolecule by at least two different modalities of scanning probe microscopy (SPM) to obtain data for one or more properties of the biomolecule;

c) analyzing the data using a model-based analysis using one or more models of physical structures of known biomolecules;

d) estimating the values of one or more parameters from the data analysis; and

e) fusing the estimated parameters to form one or more fused parameters comprising a parameter-based characterization of the biomolecule,

wherein the molecular combing comprises attachment of the biomolecule to the surface and alignment of the attached biomolecule by drawing the biomolecule through a moving meniscus.

2. (Previously Presented) The method of claim 1, wherein said fusing is based on a model of the physical structure of the biomolecule.

3. (Canceled)

4. (Previously Presented) The method of claim 1, further comprising identifying the biomolecule.

5. (Previously Presented) The method of claim 4, further comprising comparing the one or more fused parameters with parameters determined from known biomolecules to identify an occurrence of a known biomolecule.

6. (Original) The method of claim 1, wherein the SPM imaging includes at least two modalities selected from the group consisting of atomic force microscopy (AFM), scanning tunneling microscopy (STM), lateral force microscopy (LFM), chemical force microscopy (CFM), force modulation imaging, magnetic force microscopy (MFM), high frequency MFM, magnetoresistive sensitivity mapping (MSM), electric force microscopy (EFM), scanning capacitance microscopy (SCM), scanning spreading resistance microscopy (SSRM), tunneling AFM and conductive AFM.

7. (Canceled)

8. (Original) The method of claim 1, wherein the parameters are estimated by level set techniques, PDE (partial differential equation) techniques and/or active surface techniques.

9. (Original) The method of claim 8, further comprising embedding the techniques in a probabilistic (Bayesian) estimation framework to account for model uncertainty and instrument noise.

10. (Previously Presented) The method of claim 1, further comprising classifying the biomolecule by applying vector quantization, support vector machines and/or a statistical classifier to the fused parameters.

11. (Original) The method of claim 10, further comprising using known biomolecule structures to generate training sets of data.

12. (Previously Presented) The method of claim 1, further comprising using known biomolecule structures to obtain ranges of parameters for each type of biomolecule.

13. (Previously Presented) The method of claim 12, wherein the parameter ranges for known biomolecules are used in estimating the parameters.

14-23. (Canceled)

24. (Previously Presented) A molecular structure identification system comprising:

a) a surface comprising molecular structures aligned in a parallel manner by molecular combing prior to analysis;

b) a scanning probe microscope with a plurality of imaging modalities configured to obtain data for one or more properties of the molecular structures by at least two different modalities;

c) a controller to control the operation of the scanning probe microscope; and d) a memory to include one or more characterizations of known molecular structures,

wherein the molecular structures are biomolecules and the molecular combing comprises attachment of the biomolecules to the surface and alignment of the attached biomolecules by drawing the biomolecule through a moving meniscus.

25. (Original) The system of claim 24, wherein the characterizations of known structures represent sets of fused parameters derived from a plurality of known biomolecule structures.

26. (Original) The system of claim 25, wherein the characterizations of known structures are used to analyze a set of SPM images.

27. (Canceled)

28. (Previously Presented) The system of claim 26, wherein the SPM images are analyzed to identify an occurrence of one or more known structures in a sample.

29. (Original) The system of claim 28, wherein the SPM images are analyzed by (i) analyzing a coarse data set to detect locations of potential occurrences of known structures; and (ii) reanalyzing the locations of the potential occurrences one or more additional times, with each analysis utilizing a set of data that is more refined than the set of data utilized in the previous analysis.

30. (Previously Presented) The system of claim 28, wherein the plurality of imaging modalities are selected from the group consisting of atomic force microscopy (AFM), scanning tunneling microscopy (STM), lateral force microscopy (LFM), chemical force microscopy (CFM), force modulation imaging, magnetic force microscopy (MFM), high frequency MFM, magnetoresistive sensitivity mapping (MSM), electric force microscopy (EFM), scanning capacitance microscopy (SCM), scanning spreading resistance microscopy (SSRM), tunneling AFM and conductive AFM.

31. (New) The method of claim 1, wherein molecular combing comprises microfluidic molecular combing.

32. (New) The method of claim 1, wherein analyzing comprises analyzing for the presence of multiple different known biomolecules simultaneously.

33. (New) The method of claim 1, wherein analyzing comprises the three-dimensional analysis of nanoscale structures.

34. (New) The method of claim 1, wherein analyzing comprises determining a primary structure of the biomolecule.

35. (New) The method of claim 1, wherein analyzing comprises determining a secondary structure of the biomolecule.

36. (New) The method of claim 1, wherein analyzing comprises determining a tertiary structure of the biomolecule.

37. (New) The method of claim 1, wherein analyzing comprises determining a quarternary structure of the biomolecule.